

RAW SEQUENCE LISTING

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Application Serial Number: 10/073,138A
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/073,138A

DATE: 08/31/2005
TIME: 16:57:51

Input Set : A:\US10073138.txt
Output Set: N:\CRF4\08312005\J073138A.raw

3 <110> APPLICANT: ANDERSON, DARRELL R.
 4 HANNA, NABIL
 5 BRAMS, PETER
 6 HEARD, CHERYL
 8 <120> TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
 9 CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
 10 CO-STIMULATORY ANTIGENS
 12 <130> FILE REFERENCE: 37003-280705
 14 <140> CURRENT APPLICATION NUMBER: 10/073138A
 15 <141> CURRENT FILING DATE: 2002-02-13
 17 <150> PRIOR APPLICATION NUMBER: PCT/US97/19906
 18 <151> PRIOR FILING DATE: 1997-10-29
 20 <150> PRIOR APPLICATION NUMBER: 08/746,361
 21 <151> PRIOR FILING DATE: 1996-11-08
 23 <150> PRIOR APPLICATION NUMBER: 08/487,550
 24 <151> PRIOR FILING DATE: 1995-06-07
 26 <160> NUMBER OF SEQ ID NOS: 6
 28 <170> SOFTWARE: PatentIn Ver. 2.1
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 705
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Homo sapiens
 35 <220> FEATURE:
 36 <221> NAME/KEY: CDS
 37 <222> LOCATION: (1)..(702)
 39 <400> SEQUENCE: 1

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41	Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro	
42	1 5 10 15	
44	ggt gca cga tgt gcc tat gaa ctg act cag cca ccc tcg gtg tca gtg	96
45	Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val	
46	20 25 30	
48	tcc cca gga cag acg gcc agg atc acc tgt ggg gga gac aac agt aga	144
49	Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg	
50	35 40 45	
52	aat gaa tat gtc cac tgg tac cag cag aag cca gcg cgg gcc cct ata	192
53	Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile	
54	50 55 60	
56	ctg gtc atc tat gat gat agt gac cgg ccc tca ggg atc cct gag cga	240
57	Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg	
58	65 70 75 80	
60	ttc tct ggc tcc aaa tca ggg aac acc gcc acc ctg acc atc aac ggg	288
61	Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly	

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62	85	90	95	
64	gtc gag gcc ggg gag gac tat tac tgt cag gtg tgg gac agg	336		
65	Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg			
66	100 105	110		
68	gct agt gat cat ccg gtc ttc gga gga ggg acc ccg gtg acc gtc cta	384		
69	Ala Ser Asp His Pro Val Phe Gly Gly Thr Arg Val Thr Val Leu			
70	115 120	125		
72	ggt cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct	432		
73	Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser			
74	130 135	140		
76	gag gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac	480		
77	Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp			
78	145 150	155 160		
80	ttc tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc	528		
81	Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro			
82	165 170	175		
84	gtc aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac	576		
85	Val Lys Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn			
86	180 185	190		
88	aag tac gcg gcc agc agc tac ctg agc ctg acg cct gag cag tgg aag	624		
89	Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys			
90	195 200	205		
92	tcc cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg	672		
93	Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val			
94	210 215	220		
96	gag aag aca gtg gcc cct aca gaa tgt tca tga	705		
97	Glu Lys Thr Val Ala Pro Thr Glu Cys Ser			
98	225 230			
101	<210> SEQ ID NO: 2			
102	<211> LENGTH: 1431			
103	<212> TYPE: DNA			
104	<213> ORGANISM: Homo sapiens			
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108	<222> LOCATION: (1)..(1428)			
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113	1 5	10 15		
115	gtc ctg tcc cag gtg aag ctg cag cag tgg ggc gaa gga ctt ctg cag	96		
116	Val Leu Ser Gln Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln			
117	20 25	30		
119	cct tcg gag acc ctg tcc cgc acc tgc gtt gtc tct ggt ggc tcc atc	144		
120	Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile			
121	35 40	45		
123	agc ggt tac tac tac tgg acc tgg atc cgc cag acc cca ggg agg gga	192		
124	Ser Gly Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly			
125	50 55	60		
127	ctg gag tgg att ggc cat att tat ggt aat ggt gcg acc acc aac tac	240		

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128	Leu	Glu	Trp	Ile	Gly	His	Ile	Tyr	Gly	Asn	Gly	Ala	Thr	Thr	Asn	Tyr	
129	65				70				75				80				
131	aat	ccc	tcc	ctc	aag	agt	cga	gtc	acc	att	tca	aaa	gac	acg	tcc	aag	288
132	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	
133										85				95			
135	aac	cag	tcc	ttc	ctg	aac	ttg	aat	tct	gtg	acc	gac	gcg	gac	acg	gcc	336
136	Asn	Gln	Phe	Phe	Leu	Asn	Leu	Asn	Ser	Val	Thr	Asp	Ala	Asp	Thr	Ala	
137										100			105		110		
139	gtc	tat	tac	tgt	gcf	aga	ggc	cct	cgc	cct	gat	tgc	aca	acc	att	tgt	384
140	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Pro	Arg	Pro	Asp	Cys	Thr	Thr	Ile	Cys	
141										115			120		125		
143	tat	ggc	ggc	tgg	gtc	gat	gtc	tgg	ggc	ccg	gga	gac	ctg	gtc	acc	gtc	432
144	Tyr	Gly	Gly	Trp	Val	Asp	Val	Trp	Gly	Pro	Gly	Asp	Leu	Val	Thr	Val	
145										130			135		140		
147	tcc	tca	gct	agc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca	ccc	tcc	480
148	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	
149	145									150			155		160		
151	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcf	gcc	ctg	ggc	tgc	ctg	gtc	aag	528
152	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
153										165			170		175		
155	gac	tac	tcc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	576
156	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
157										180			185		190		
159	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	624
160	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
161										195			200		205		
163	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	672
164	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
165										210			215		220		
167	cag	acc	tac	atc	tcg	aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	720
168	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	
169	225									230			235		240		
171	gac	aag	aaa	gca	gag	ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	768
172	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	
173										245			250		255		
175	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	816
176	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	
177										260			265		270		
179	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cg	acc	cct	gag	gtc	864
180	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	
181										275			280		285		
183	aca	tgc	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc		912
184	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	
185										290			295		300		
187	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	960
188	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
189	305									310			315		320		
191	cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	1008
192	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	

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193	325	330	335	
195	gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc			1056
196	Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val			
197	340	345	350	
199	tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc			1104
200	Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala			
201	355	360	365	
203	aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg			1152
204	Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg			
205	370	375	380	
207	gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc			1200
208	Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly			
209	385	390	395	400
211	ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg			1248
212	Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro			
213	405	410	415	
215	gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc			1296
216	Glu Asn Asn Tyr Lys Thr Pro Pro Val Leu Asp Ser Asp Gly Ser			
217	420	425	430	
219	ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag			1344
220	Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln			
221	435	440	445	
223	ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac			1392
224	Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His			
225	450	455	460	
227	tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga			1431
228	Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys			
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232	<210> SEQ ID NO: 3			
233	<211> LENGTH: 720			
234	<212> TYPE: DNA			
235	<213> ORGANISM: Homo sapiens			
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238	<221> NAME/KEY: CDS			
239	<222> LOCATION: (1)..(717)			
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244	1	5	10	15
246	ggg tcc agt ggg gaa gtt gtg atg act cag tct cca ctg tcc ctt ccc			96
247	Gly Ser Ser Gly Glu Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro			
248	20	25	30	
250	atc aca cct gga gag ccg gcc tcc atc tcc tgt agg tct agt caa agc			144
251	Ile Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser			
252	35	40	45	
254	ctt aaa cac agt aat gga gac acc ttc ctg agt tgg tat cag cag aag			192
255	Leu Lys His Ser Asn Gly Asp Thr Phe Leu Ser Trp Tyr Gln Gln Lys			
256	50	55	60	
258	cca ggc caa cct cca agg ctc ctg att tat aag gtt tct aac ccg gac			240

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259 Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Asp
260 65 70 75 80
262 tct ggg gtc cca gac aga ttc agc ggc agt ggg gca ggg aca gat ttc 288
263 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe
264 85 90 95
266 aca ctg aaa atc agc gca gtg gag gct gaa gat gtt ggg gtt tat ttc 336
267 Thr Leu Lys Ile Ser Ala Val Glu Ala Glu Asp Val Gly Val Tyr Phe
268 100 105 110
270 tgc ggg caa ggt aca agg act cct ccc act ttc ggc gga ggg acc aag 384
271 Cys Gly Gln Gly Thr Arg Thr Pro Pro Thr Phe Gly Gly Thr Lys
272 115 120 125
274 gtg gaa atc aaa cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg 432
275 Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
276 130 135 140
278 cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg 480
279 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
280 145 150 155 160
282 ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat 528
283 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
284 165 170 175
286 aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac 576
287 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
288 180 185 190
290 agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa 624
291 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
292 195 200 205
294 gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 672
295 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
296 210 215 220
298 ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tga 720
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300 225 230 235
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315 1 5 10 15
317 gtc cag tgt gag gtg caa ctg gtg gag tct ggg gga ggc ttg gtc cag 96
318 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln
319 20 25 30
321 cct ggc ggg tcc ctg aga gtc tcc tgt gca gtc tct gga ttc acc ttc 144
322 Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Val Ser Gly Phe Thr Phe
323 35 40 45

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